

#6
NB
11/14/95RAW SEQUENCE LISTING
PATENT APPLICATION US/08/482,785DATE: 10/27/95
TIME: 09:47:56

INPUT SET: S6937.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Adams, Craig W.
6 Pang, Patty P.-Y.
7 Belei, Marina
8
9 (ii) TITLE OF INVENTION: Recombinant DNase B Derived from
10 Streptococcus pyogenes
11
12 (iii) NUMBER OF SEQUENCES: 16
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Sheldon & Mak
16 (B) STREET: 225 South Lake Avenue, Ninth Floor
17 (C) CITY: Pasadena
18 (D) STATE: California
19 (E) COUNTRY: USA
20 (F) ZIP: 91001
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: US 08/482,785
30 (B) FILING DATE: 07-JUN-1995
31 (C) CLASSIFICATION: 435
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: US/08/393,889
35 (B) FILING DATE: 24-FEB-1995
36
37 (A) APPLICATION NUMBER: US/08/082,845
38 (B) FILING DATE:
39
40 (viii) ATTORNEY/AGENT INFORMATION:
41 (A) NAME: Farber, Michael B.
42 (B) REGISTRATION NUMBER: 32,612
43 (C) REFERENCE/DOCKET NUMBER: 9521
44
45 (ix) TELECOMMUNICATION INFORMATION:
46 (A) TELEPHONE: (818) 796-4000

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/482,785DATE: 10/27/95
TIME: 09:48:00

INPUT SET: S6937.raw

(B) TELEFAX: (818) 795-6321

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pyogenes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Asn	Leu	Leu	Gly	Ser	Arg	Arg	Val	Phe	Ser	Lys	Lys	Cys	Arg	Leu
1				5					10					15	

Val	Lys	Phe	Ser	Met	Val	Ala	Leu	Val	Ser	Ala	Thr	Met	Ala	Val	Thr
			20					25					30		

Thr	Val	Thr	Leu	Glu	Asn	Thr	Ala	Leu	Ala	Arg
			35				40			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Synthetic DNA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/482,785DATE: 10/27/95
TIME: 09:48:05INPUT SET: S6937.raw
41

100 TAACGGATCC GAATCTACTT GGATCAAGAC GGGTTTTTTC T

101

102 (2) INFORMATION FOR SEQ ID NO:3:

103

104 (i) SEQUENCE CHARACTERISTICS:

105 (A) LENGTH: 41 base pairs

106 (B) TYPE: nucleic acid

107 (C) STRANDEDNESS: single

108 (D) TOPOLOGY: linear

109

110 (ii) MOLECULE TYPE: DNA (genomic)

111

112 (iii) HYPOTHETICAL: NO

113

114 (iv) ANTI-SENSE: NO

115

116 (vi) ORIGINAL SOURCE:

117 (A) ORGANISM: Synthetic DNA primer

118

119

120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

121

122 CCGGGTCGAC CCGGGGAATG ACGGCAATCA TTGCTTTTTC T

41

123

124 (2) INFORMATION FOR SEQ ID NO:4:

125

126 (i) SEQUENCE CHARACTERISTICS:

127 (A) LENGTH: 23 amino acids

128 (B) TYPE: amino acid

129 (D) TOPOLOGY: linear

130

131 (ii) MOLECULE TYPE: peptide

132

133 (iii) HYPOTHETICAL: NO

134

135 (v) FRAGMENT TYPE: N-terminal

136

137 (vi) ORIGINAL SOURCE:

138 (A) ORGANISM: Streptococcus pyogenes

139

140

141 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

142

143 Gln Thr Gln Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser Xaa

144 1 5 10 15

145

146

147 Tyr Leu Asn Glu Ala Leu Ala

148 20

149

150 (2) INFORMATION FOR SEQ ID NO:5:

151

152 (i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/482,785DATE: 10/27/95
TIME: 09:48:09

INPUT SET: S6937.raw

153 (A) LENGTH: 22 base pairs
154 (B) TYPE: nucleic acid
155 (C) STRANDEDNESS: single
156 (D) TOPOLOGY: linear

157
158 (ii) MOLECULE TYPE: DNA (genomic)
159

160 (iii) HYPOTHETICAL: NO
161

162 (iv) ANTI-SENSE: NO
163

164 (vi) ORIGINAL SOURCE:
165 (A) ORGANISM: Synthetic probe
166

167
168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
169

170 CAUACNCART NWSNAAYGAY GT 22
171

172

173 (2) INFORMATION FOR SEQ ID NO:6:
174

175 (i) SEQUENCE CHARACTERISTICS:
176 (A) LENGTH: 38 amino acids
177 (B) TYPE: amino acid
178 (D) TOPOLOGY: linear
179

180 (ii) MOLECULE TYPE: peptide
181

182 (iii) HYPOTHETICAL: NO
183

184 (v) FRAGMENT TYPE: N-terminal
185

186 (vi) ORIGINAL SOURCE:
187 (A) ORGANISM: Streptococcus pyogenes
188
189

190

191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
192

193 Arg Gln Thr Gln Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser
194 1 5 10 15
195

196

197 Lys Tyr Leu Asn Glu Ala Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn
198 20 25 30
199

200

201 Tyr Tyr Lys Thr Leu Gly
202 35
203

204

205 (2) INFORMATION FOR SEQ ID NO:7:

RAW SEQUENCE LISTING PATENT APPLICATION US/08/482,785

DATE: 10/27/95
TIME: 09:48:13

INPUT SET: S6937.raw

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206      (i) SEQUENCE CHARACTERISTICS:
207          (A) LENGTH: 1083 base pairs
208          (B) TYPE: nucleic acid
209          (C) STRANDEDNESS: double
210          (D) TOPOLOGY: linear
211
212      (ii) MOLECULE TYPE: DNA (genomic)
213
214      (iii) HYPOTHETICAL: NO
215
216      (iv) ANTI-SENSE: NO
217
218      (vi) ORIGINAL SOURCE:
219          (A) ORGANISM: Streptococcus pyogenes
220
221      (ix) FEATURE:
222          (A) NAME/KEY: CDS
223          (B) LOCATION: 129..944
224
225
226      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
227
228      GACAACGCCT TCTTTTTTCT CTTACTATC TCCTTTAATT TTCATATTTT TAAAAAAAC      60
229
230      TATTGATAAA CTAGTTAAGT AAGCGTATAC TATGGTTAGT TAGCGAAATT AGAAAAGAGG      120
231
232      ACAAGCAT ATG AAT CTA CTT GGA TCA AGA CGG GTT TTT TCT AAA AAA TGT      170
233          Met Asn Leu Leu Gly Ser Arg Arg Val Phe Ser Lys Lys Cys
234              1              5              10
235
236      CGG CTA GTA AAA TTT TCA ATG GTA GCT CTT GTA TCA GCC ACA ATG GCT      218
237      Arg Leu Val Lys Phe Ser Met Val Ala Leu Val Ser Ala Thr Met Ala
238          15              20              25              30
239
240      GTA ACA ACA GTC ACA CTT GAA AAT ACT GCA CTG GCA CGA CAA ACA CAG      266
241      Val Thr Thr Val Thr Leu Glu Asn Thr Ala Leu Ala Arg Gln Thr Gln
242              35              40              45
243
244      GTC TCA AAT GAT GTT GTT CTA AAT GAT GGC GCA AGC AAG TAC CTA AAC      314
245      Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser Lys Tyr Leu Asn
246              50              55              60
247
248      GAA GCA TTA GCT TGG ACA TTC AAT GAC AGT CCT AAC TAT TAC AAA ACT      362
249      Glu Ala Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn Tyr Tyr Lys Thr
250              65              70              75
251
252      TTA GGT ACT AGT CAG ATT ACT CCA GCA CTC TTT CCT AAA GCA GGA GAT      410
253      Leu Gly Thr Ser Gln Ile Thr Pro Ala Leu Phe Pro Lys Ala Gly Asp
254              80              85              90
255
256      ATT CTC TAT AGC AAA TTA GAT GAG TTA GGA AGG ACG CGT ACT GCT AGA      458
257      Ile Leu Tyr Ser Lys Leu Asp Glu Leu Gly Arg Thr Arg Thr Ala Arg
258              95              100              105              110

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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/482,785

DATE: 10/27/95
TIME: 09:48:17

INPUT SET: S6937.raw

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Original Text